

FIG 1

1
CCG CTC ACA TTG GGA TTC GTC ATT CTT CTT CTA AAA CCC GCA AAA TTT CTC CAT TTC TAC
61
CAA AAA TAT CCA ACT TTT ACT TTT CTT TCC TGT GAA ATT ATC TGC TCA AAT CTT TGG TTC
121
CTG ACG GAG ATG GCG GCG ATT TCA GGC ATC TCC TCT GGT ACG TIG ACG ATT TCA CGG CCT
M A A I S G I S S G T L T I S R P
181
TTG GTT ACT CTT CGA CGC TCT AGA GCC GCC GTT TCG TAC AGC TCC TCT CAC CGA TTG CTT
L V T L R R S R A A V S Y S S S H R L L
241
CAT CAT CTT CCT CTC TCT TCT CGT CGT CTG CTA TTA AGG AAC AAT CAT CGA GTC CAA GCA
H H L P L S S R R L L L R N N H R V O * A
301
ACG ATT TTG CAA GAC GAT GAA GAG AAA GTG GTG GTG GAG GAA TCG TTT AAA GCC GAG ACT
T I L Q D D E E K V V V E E S F K A E T
361
TCT ACT GGT ACA GAA CCA CTT GAG GAG CCA AAT ATG AGT TCT TCT TCA ACT AGT GCT TTT
S T G T E P L E E P N M S S S S T S A F
421
GAG ACA TGG ATC ATC AAG CTT GAG CAA GGA GTG AAT GTT TTC CTT ACA GAC TCG GTT ATT
E T W I I K L E Q G V N V F L T D S V I
481
AAG ATA CTT GAC ACT TTG TAT CGT GAC CGA ACA TAT GCA AGG TTC TTT GTT CTT GAG ACA
K I L D T L Y R D R T Y A R F F V L E T
541
ATT GCT AGA GTG CCT TAT TTT GCG TTT ATG TCT GTG CTA CAT ATG TAT GAG ACC TTT GGT
I A R V P Y F A F M S V L H M Y E T F G
601
TGG TGG AGG AGA GCA GAT TAT TTG AAA GTA CAC TTT GCT GAG AGC TGG AAT GAA ATG CAT
W W R R A D Y L K V H F A E S W N E M H
661
CAC TTG CTC ATA ATG GAA GAA TTG GGT GGA AAT TCT TGG TGG TTT GAT CGT TTT CTG GCT
H L L I M E E L G G N S W W F D R F L A
721
CAG CAC ATA GCA ACC TTC TAC TAC TTC ATG ACA GTG TTC TTG TAT ATC TTA AGC CCT AGA
Q H I A T F Y Y F M T V F L Y I L S P R
781
ATG GCA TAT CAC TTT TCG GAA TGT GTG GAG AGT CAT GCA TAT GAG ACT TAT GAT AAA TTT
M A Y H F S E C V E S H A Y E T Y D K F
841
CTC AAG GCC AGT GGA GAG GAG TTG AAG AAT ATG CCT GCA CCG GAT ATC GCA GTA AAA TAC
L K A S G E E L K N M P A P D I A V K Y
901
TAT ACG GGA GGT GAC TTG TAC TTA TTT GAT GAG TTC CAA ACA TCA AGA ACT CCC AAT ACT
Y T G G D L Y L F D E F Q T S R T P N T
961
CGA AGA CCA GTA ATA GAA AAT CTA TAC GAT GTG TTT GTG AAC ATA AGA GAT GAT GAA GCA
R R P V I E N L Y D V F V N I R D D E A
1021
GAA CAC TGC AAG ACA ATG AGA GCT TGT CAG ACT CTA GGC AGT CTG CGT TCT CCA CAC TCC
E H C K T M R A C Q T L G S L R S P H S
1081
ATT TTA GAT GAT GAT GAT ACT GAA GAA GAA TCA GGG TGT GTT GTT CCT GAG GAG GCT CAT
I L D D D D T E E E S G C V V P E E A H
1141
TGC GAA GGT ATT GTA GAC TGC CTC AAG AAA TCC ATT ACA AGT TAA TAA ATT AGA AAG TAA
C E G I V D C L K K S I T S
1201
ACT AAA AAA GAT TAT TTG TAT CAG CTC ATG AAC AAT AGA TAT AAT CCC ATA TAC TTG GGA
1261
ATA AAG GAA TAA TGT GAA ATT CCC ATC GTT GTG CTA GTG TGT GAG AGA ATC AAA TAC CCT
1321
AAT GAT GTA AAT GTA CTT TGA TGA GCT TAA GTC GTT GTA GAC CAT TTT ATC AAA AAA AAA
1381
AAA AAA AAA AAA AAA A

TOP SECRET 233605

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FIG 2

IMM : 111 FLTDSVIKILDTLYRDRTYA-REFVLEMLAR/PVFAFMSVEHMYETFGWRRRADYLVKVF 169
+ T +++I L+ R Y R +LET+A VP +LH+ + + ++K
AOX : 136 YRTVKLLRIPTDLEFFKRRYGCRAMMGENTVAVEGMMGGMHLRLSLRKFQQSGGWIKALL 195
IMM : 170 AESWNEMHLLIMEELGCNSWFDRELAQHIALEFVZMMVLEMLLSPRMAYHFSECVES 229
E+ NE HL+ M EL W++R L + ++ LYILSP++A+ +E
AOX : 196 EEAENERMHLMTMVEL-VKPKWYERLEMLAVOGVFEENAFVAYILSPKVAHRIVGYLEEE 254
IMM : 230 AYETYDKFLK-ASGEELKNMPAPDIAVKYYTGDDLVLDFDEFQTSRTPTNTRRPVLENLYDV 288
A +Y ++LK ++N+PAP IA+ Y+ R P L DV
AOX : 255 AIHSYTEYLKDLLESGAIENVPAPAIAIDYW-----RLPKDARLKDV 295
IMM : 289 FVNIRDDEAEH 299
IR DEA H
AOX : 296 ITVIRADEAAH 306

FIG 3

```
T 1 MAISISAMSGTSTVSSYSCEFRRSFEKSSVLCNSQNPCRFNSVFP.IRKSDGASRCSVSR
P 1 MAISISAMSFRTSTVSS.....SY..SAFLCNSKNPFCLNSLFS.LRNSHRTFQPSLSR
A 1 MA.AISGISSGTLTIS.....RPLVTLRRSRAAVSYSSSHRLLHHLPLSSRLLLLR
```

consensus

1 MA ISamS T S L S S 1r 1 R

T 60 KSCRVRATLLQENEEVVVEKSFAPKSFDPNVGGGSNGKPPDDSSS.NGLEKWVIKLEQS
P 51 KSSRV RATLLKENEEVVVEKSFAPKSFPGNVGGGNNGEPPDNSSS.NGLEKWVIKIEQS
A 51 NNHRVOATILQDDEEKVVVEESFKAEE...TSTGTEPLEEPNMSSSSSTSAFETWIIKLEQG

consensus

61 RV AT1L e EE VVVE SF G P SSS g E WvIKiEQ

T 119 VNILLTDSVIKILD TLYHNRNYARFFVLETIARVPYFAFISVLHMYESFGWWRADYMKV
P 110 VNIFLTDSVIKILD TLYHDRHYARFFVLETIARVPYFAFISVLHLYESFGWWRADYMKV
A 108 VNVFLTDSVIKILD TLYRDRTYARFFVLETIARVPYFAFMSVLHMYETFGWWRADYMKV

consensus

121 VNj LTDSVIKILDTLYh R YARFFVLETIARVPYFAFISVLHLYEgFGWWRRADYlKV

T 179 HFAESWNEMHLLIMEELGGNAWWFDRFLAQHIAIFYYFMTVLMYALSPRMAYHFSECVE
P 170 HFAESWNEMHLLIMEELGGNAWWFDRFLAQHIAVFYYFMTVSMYALSPRMAYHFSECVE
A 168 HFAESWNEMHLLIMEELGGNSWWFDRFLAQHIATFYYFMTVFLYILSPRMAYHFSECVE

Consensus

181 HFAESWNEHLLIMEELGGN WWFDRFLAQHIA FYYFMTV mY LSPRMAYHFSECVE

T 239 SHAYETYDKFIKDQGEELKNLPAPKIAVDYYTGGDLYLFDEFQTSREPNTRRPKIDNLYD
P 230 HHAYETYDKFIKDQEAELKKLPAPKIAVSYYTGGDLYLFDEFQTSREPNTRRPKIDNLYD
A 227 SHAYETYDKFLKASGEELKNMPAPDIAVKYYTGGDLYLFDEFQTSRTPNTRRPVIENTLYD

Consensus

241 HAYETYDKFik ELK lPAP IAV YYTGGLDLYLFDEFQTSR PNTRRP IdNLYD

T 299 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTD.PCDDSEDDTGCSVP.QADCIGIVDCIKK
P 290 VFMNIRDDEAEHCKTMKACQTHGSLRSPHTN.PCDESEDDPGCSVP.QADCVGIVDCITK
A 287 VVFNIRDDEAEHCKTMRACQTLGSLRSPHSILDDDDTEEESGCVVPEEAHCEGIVDCLKK

Consensus

301 VFmNIRDDEAEHCKTMkACQT GSLRSPHT DdsEdd GC VP A C GIVDCi K

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FIG 3 (suite)

T 357 SVTDTQVTKR

P 348 SVADPNVGRR

A 347 SITS.....

Consensus

361 Sv

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FIG 4

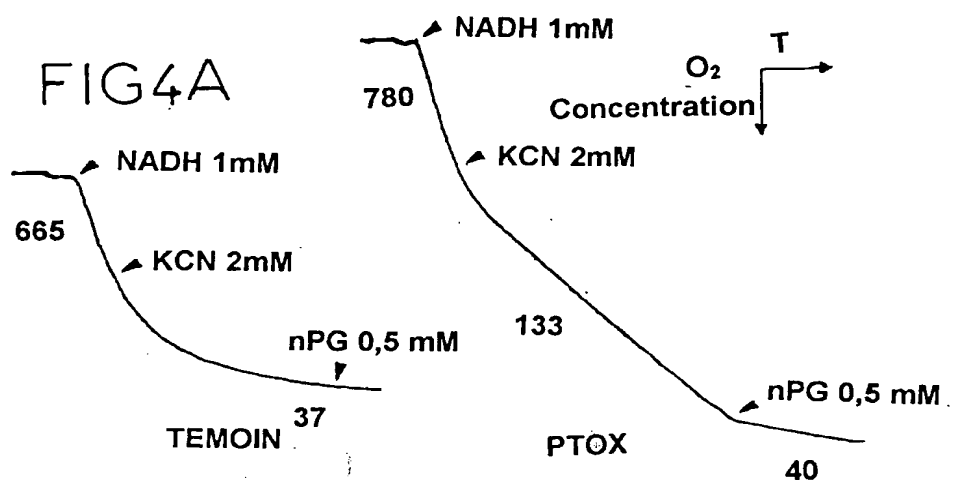


FIG 4B

